Claims 1-10 (canceled):

Claim 11 (currently amended): A PR-39 derived oligopeptide family whose members individually cause a selective inhibition of proteasome-mediated degradation [of a specific peptide] in-situ after introduction intracellularly to a viable cell, each member of said PR-39 derived oligopeptide family being

an oligopeptide which is pharmacologically active and is less than 26 amino acid residues in length;

an oligopeptide whose N-terminal amino acid residue sequence begins with Arg-Arg-Arg;

an oligopeptide which is an analog of the amino acid sequence of native PR-39 peptide;

an oligopeptide able to selectively alter [which is pharmacologically active for selectively altering] the proteolytic degradation activity of proteasomes in-situ;

an oligopeptide able to interact in-situ with at least the $\alpha 7$ subunit of such proteasomes as are present within the cytoplasm of the cell; and

an oligopeptide able selectively to alter the proteolytic degradation activity of said proteasomes having an interacting $\alpha 7$ subunit such that the proteolytic degradation mediated by said proteasomes against [a specific peptide] at least one peptide selected from the group consisting of IκBα and

HIF-1α becomes selectively inhibited [while the] without substantially altering other proteolytic degradation mediated by said proteasomes [apart from against said specific peptide remains unaltered].

Claim 12 (previously presented): The PR-39 derived oligopeptide family as recited in claim 11 or 15 whose membership includes a peptide comprised of 15 amino acid residues whose sequence is Arg-Arg-Arg-Pro-Arg-Pro-Pro-Tyr-Leu-Pro-Arg-Pro-Arg-Pro-Pro (SEQ ID NO: 3).

Claim 13 (previously presented): The PR-39 derived oligopeptide family as recited in claim 11 or 15 whose membership includes a peptide comprised of 11 amino acid residues whose sequence is Arg-Arg-Arg-Pro-Arg-Pro-Pro-Tyr-Leu-Pro-Arg (SEQ ID NO: 4).

Claim 14 (previously presented): The PR-39 derived oligopeptide family as recited in claim 11 or 15 whose membership includes a peptide comprised of 8 amino acid residues whose sequence is Arg-Arg-Arg-Pro-Arg-Pro-Pro-Tyr (SEQ ID NO: 5).

Claim 15 (currently amended): A PR-39 derived oligopeptide family whose members cause a selective inhibition of protease-mediated

degradation [of a specific peptide] in-situ after introduction intracellularly to a viable cell, each member of said PR-39 oligopeptide family being:

an oligopeptide which is pharmacologically active and is less than 20 amino acid residues in length;

an oligopeptide whose N-terminal amino acid residue sequence begins with Arg-Arg-Arg;

an oligopeptide which is an analog of the amino acid sequence of native PR-39 peptide;

an oligopeptide able to selectively alter [which is pharmacologically active for selectively altering] the proteolytic degradation activity of proteasomes in-situ;

an oligopeptide able to interact in-situ with at least the α7 subunit of such proteasomes as are present within the cytoplasm of the cell; and

an oligopeptide able selectively to alter the proteolytic degradation activity of said proteasomes having an interacting α7 subunit such that the proteolytic degradation mediated by said proteasomes against [a specific peptide] at least one peptide selected from the group consisting of IκBα and HIF-1α becomes selectively inhibited [while the] without substantially altering other proteolytic degradation mediated by said proteasomes [apart from against said specific peptide remains unaltered].